

Revised

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/836,455DATE: 06/23/98
TIME: 13:34:14

INPUT SET: S26895.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: Chatterjee, Malaya
6 Foon, Kenneth A.
7 Chatterjee, Sunil K.
8
9 (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
10 11D10 AND METHODS OF USE THEREOF
11
12 (iii) NUMBER OF SEQUENCES: 59
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: MORRISON & FOERSTER
16 (B) STREET: 755 PAGE MILE ROAD
17 (C) CITY: PALO ALTO
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 94304-1018
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US 08/836,455
30 (B) FILING DATE: 09-MAY-1997
31 (C) CLASSIFICATION:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: Polizzi, Catherine M.
35 (B) REGISTRATION NUMBER: 40,130
36 (C) REFERENCE/DOCKET NUMBER: 30414-20003.22
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: (650) 813-5600
40 (B) TELEFAX: (650) 494-0792
41 (C) TELEX: 706141
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 435 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear

51
52 (ii) MOLECULE TYPE: DNA (genomic)

53
54
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 1..435

58
59 (ix) FEATURE:
60 (A) NAME/KEY: mat_peptide
61 (B) LOCATION: 61

62
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

64 ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 48
65 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
66 -20 -15 -10 -5
67
68
69 GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT 96
70 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
71 1 5 10
72
73 GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 144
74 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
75 15 20 25
76
77 ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 192
78 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
79 30 35 40
80
81 AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 240
82 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
83 45 50 55 60
84
85 AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288
86 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
87 65 70 75
88
89 AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336
90 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
91 80 85 90
92
93 AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384
94 Ser Ser Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
95 95 100 105
96
97 GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT 432
98 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
99

**RAW SEQUENCE LISTING
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100 110 115 120 435
101
102 GGG
103 Gly
104 125
105
106
107 (2) INFORMATION FOR SEQ ID NO:2:
108
109 (i) SEQUENCE CHARACTERISTICS:
110 (A) LENGTH: 145 amino acids
111 (B) TYPE: amino acid
112 (D) TOPOLOGY: linear
113
114 (ii) MOLECULE TYPE: protein
115
116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
117
118 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro
119 -20 -15 -10 -5
120
121 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
122 1 5 10
123
124 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
125 15 20 25
126
127 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
128 30 35 40
129
130 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
131 45 50 55 60
132
133 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
134 65 70 75
135
136 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
137 80 85 90
138
139 Ser Ser Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
140 95 100 105
141
142 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
143 110 115 120
144
145 Gly
146 125
147
148 (2) INFORMATION FOR SEQ ID NO:3:
149
150 (i) SEQUENCE CHARACTERISTICS:
151 (A) LENGTH: 461 base pairs
152 (B) TYPE: nucleic acid

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153 (C) STRANDEDNESS: single
154 (D) TOPOLOGY: linear
155
156 (ii) MOLECULE TYPE: DNA (genomic)
157
158
159 (ix) FEATURE:
160 (A) NAME/KEY: CDS
161 (B) LOCATION: 1..459
162
163 (ix) FEATURE:
164 (A) NAME/KEY: mat_peptide
165 (B) LOCATION: 58
166
167
168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
169
170 ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT 48
171 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
172 -19 -15 -10 -5
173
174 GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG 96
175 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
176 1 5 10
177
178 TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG 144
179 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
180 15 20 25
181
182 ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG 192
183 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
184 30 35 40 45
185
186 GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT 240
187 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
188 50 55 60
189
190 CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC 288
191 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
192 65 70 75
193
194 ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC 336
195 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
196 80 85 90
197
198 TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT 384
199 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
200 95 100 105
201
202 CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC 432
203 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
204 110 115 120 125
205

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206 GTC TAT CCA CTG GTC CCT GGA AGC TTG GG
207 Val Tyr Pro Leu Val Pro Gly Ser Leu
208 130

209

210

211 (2) INFORMATION FOR SEQ ID NO:4:

212

213 (i) SEQUENCE CHARACTERISTICS:
214 (A) LENGTH: 153 amino acids
215 (B) TYPE: amino acid
216 (D) TOPOLOGY: linear

217

218 (ii) MOLECULE TYPE: protein

219

220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

221

222 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
223 -19 -15 -10 -5

224

225 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
226 1 5 10

227

228 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
229 15 20 25

230

231 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
232 30 35 40 45

233

234 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
235 50 55 60

236

237 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
238 65 70 75

239

240 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
241 80 85 90

242

243 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
244 95 100 105

245

246 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
247 110 115 120 125

248

249 Val Tyr Pro Leu Val Pro Gly Ser Leu
250 130

251

252 (2) INFORMATION FOR SEQ ID NO:5:

253

254 (i) SEQUENCE CHARACTERISTICS:
255 (A) LENGTH: 321 base pairs
256 (B) TYPE: nucleic acid
257 (C) STRANDEDNESS: single
258 (D) TOPOLOGY: linear

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SEQUENCE VERIFICATION REPORT
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Original Text